

#8

1648

Raw Seq List #

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/509,239

DATE: 01/30/2001
 TIME: 10:47:56

Input Set : A:\seqlist.txt
 Output Set: N:\CRF3\01302001\I509239.raw

4 <110> APPLICANT: Bruck, Claudine
 5 Godart, Stephane Andre Georges
 6 Marc-Hand, Martine
 8 <120> TITLE OF INVENTION: Fusion Proteins Comprising HIV-1 TAT
 9 and/or Nef Proteins
 11 <130> FILE REFERENCE: B45110
 13 <140> CURRENT APPLICATION NUMBER: 09/509,239
 14 <141> CURRENT FILING DATE: 2000-03-23
 16 <150> PRIOR APPLICATION NUMBER: PCT/EP98/06040
 17 <151> PRIOR FILING DATE: 1998-09-17
 19 <150> PRIOR APPLICATION NUMBER: GB 9720585.0
 20 <151> PRIOR FILING DATE: 1997-09-26
 22 <160> NUMBER OF SEQ ID NOS: 27
 24 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 23
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Pichia pastoris
 31 <400> SEQUENCE: 1
 32 atcgtccatg ggtggcaagt ggt 23
 34 <210> SEQ ID NO: 2
 35 <211> LENGTH: 23
 36 <212> TYPE: DNA
 37 <213> ORGANISM: Pichia pastoris
 39 <400> SEQUENCE: 2
 40 cygctactag tgcagttctt gaa 23
 42 <210> SEQ ID NO: 3
 43 <211> LENGTH: 24
 44 <212> TYPE: DNA
 45 <213> ORGANISM: Pichia pastoris
 47 <400> SEQUENCE: 3
 48 atcgtactag tgagccagta gac 24
 50 <210> SEQ ID NO: 4
 51 <211> LENGTH: 24
 52 <212> TYPE: DNA
 53 <213> ORGANISM: Pichia pastoris
 55 <400> SEQUENCE: 4
 56 cygctactag ttctcttcgg gcct 24
 58 <210> SEQ ID NO: 5
 59 <211> LENGTH: 23
 60 <212> TYPE: DNA
 61 <213> ORGANISM: Pichia pastoris
 63 <400> SEQUENCE: 5
 64 atcgtccatg gagccagtag atc 23
 66 <210> SEQ ID NO: 6
 67 <211> LENGTH: 441
 68 <212> TYPE: DNA

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72 atggatccaa aaactttaqc cctttcttta ttagcagctg gcgtactagc aggtttgtagc 60
73 agccattcat caaatatggc gaatacccaa atgaaatcag acaaaatcat tattgctcac 120
74 cgtggtgcta gcggttatatt accagagcat acgttagaat cttaaagcact tgcttttgca 180
75 caacaggetg attatttaga gcaagattta gcaatgacta aggatggtcy tttagtggtt 240
76 attcacgata actttttaga tggcttgact gatgttgcga aaaaattccc acatcgtcat 300
77 cgtaaagatg gccgttacta tgtcatcgac tttacottaa aagaaattca aagtttagaa 360
78 atgacagaaa actttgaaac catggccacg tgtgatcaga gctcaactag tggccaccat 420
79 caccatcacc attaatctag a 441
81 <210> SEQ ID NO: 7
82 <211> LENGTH: 144
83 <212> TYPE: PRT
84 <213> ORGANISM: Pichia pastoris
86 <400> SEQUENCE: 7
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88 1 5 10 15
89 Ala Gly Cys Ser Ser His Ser Ser Asn Met Ala Asn Thr Gln Met Lys
90 20 25 30
91 Ser Asp Lys Ile Ile Ile Ala His Arg Gly Ala Ser Gly Tyr Leu Pro
92 35 40 45
93 Glu His Thr Leu Glu Ser Lys Ala Leu Ala Phe Ala Gln Ala Asp
94 50 55 60
95 Tyr Leu Glu Gln Asp Leu Ala Met Thr Lys Asp Gly Arg Leu Val Val
96 65 70 75 80
97 Ile His Asp His Phe Leu Asp Gly Leu Thr Asp Val Ala Lys Lys Phe
98 85 90 95
99 Pro His Arg His Arg Lys Asp Gly Arg Tyr Tyr Val Ile Asp Phe Thr
100 100 105 110
101 Leu Lys Glu Ile Gln Ser Leu Glu Met Thr Glu Asn Phe Glu Thr Met
102 115 120 125
103 Ala Thr Cys Asp Gln Ser Ser Thr Ser Gly His His His His His
104 130 135 140
106 <210> SEQ ID NO: 8
107 <211> LENGTH: 648
108 <212> TYPE: DNA
109 <213> ORGANISM: Pichia pastoris
111 <400> SEQUENCE: 8
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113 agacgagctg agccagcagc agatgggggt ggagcagcat ctcgagacct ggaaaaacat 120
114 ggagcaatca caagtagcaa tacagcagct accaatgctg cttgtgctg gctagaagca 180
115 caagaggagg aggaggtggg ttttcagtc acacctcagg tacctttaag accaatgact 240
116 tacaaggcag ctgtagatct tagccacttt ttaaaagaaa aggggggact ggaagggcta 300
117 attcactccc aacgaagaca agatatacct gatctgtgga tctaccacac acaaggctac 360
118 ttccctgatt ggcagaacta cacaccaggg ccaggggtca gatataccact gaccttttga 420
119 tgggtgctaca agctagtacc agttgagcca gataaggtag aagaggccaa taaaggagag 480
120 aacaccagct tgttacaccc tgtgagcctg catggaatgg atgacctga gagagaagtg 540
121 ttagagtgga ggtttgacag ccgcctagca ttcatcacg tggcccgaga gctgcatccg 600
122 gagtacttca agaactgcac tagtgccac catcaccatc accattaa 648

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124 <210> SEQ ID NO: 9
125 <211> LENGTH: 215
126 <212> TYPE: PRT
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129 <400> SEQUENCE: 9
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132 Arg Glu Arg Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly Ala
133 20 25 30
134 Ala Ser Arg Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn Thr
135 35 40 45
136 Ala Ala Thr Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu
137 50 55 60
138 Glu Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr
139 65 70 75 80
140 Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly
141 85 90 95
142 Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu
143 100 105 110
144 Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr
145 115 120 125
146 Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys
147 130 135 140
148 Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu
149 145 150 155 160
150 Asn Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp Asp Pro
151 165 170 175
152 Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His
153 180 185 190
154 His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser
155 195 200 205
156 Gly His His His His His His
157 210 215
159 <210> SEQ ID NO: 10
160 <211> LENGTH: 288
161 <212> TYPE: DNA
162 <213> ORGANISM: Pichia pastoris
164 <400> SEQUENCE: 10
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166 gcttgtagca attgctattg taaaaagtgt tgctttcatt gccaaagttg ttccataaca 120
167 aaagccttag gcatctccta tggcagggaag aagcggagac agcgacgaag acctcctcaa 180
168 ggcagtcaga ctcatcaagt ttctctatca aagcaaccca cctcccaatc ccgaggggac 240
169 ccgacaggcc cgaaggaaac tagtggccac catcaccatc accatttaa 288
171 <210> SEQ ID NO: 11
172 <211> LENGTH: 95
173 <212> TYPE: PRT
174 <213> ORGANISM: Pichia pastoris
176 <400> SEQUENCE: 11
177 Met Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser

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178      1          5          10          15
179 Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe
180                20                25                30
181 His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly
182                35                40                45
183 Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr
184                50                55                60
185 His Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Arg Gly Asp
186 65                70                75                80
187 Pro Thr Gly Pro Lys Glu Thr Ser Gly His His His His His His
188                85                90                95
190 <210> SEQ ID NO: 12
191 <211> LENGTH: 909
192 <212> TYPE: DNA
193 <213> ORGANISM: Pichia pastoris
194 <400> SEQUENCE: 12
196 atgggtgqca agtgggtcaaa aagttagtgtg gttggatggc ctactgtaag ggaaagaatg      60
197 agacgagctg agccagcagc agatggggty ggagcagcat ctcgagacct ggaaaaacat      120
198 ggagcaatca caagtagcaa tacagcagct accaatgctg cttgtgcctg gctagaagca      180
199 caagaggagg aggaggtggg tttccagtc acacctcagg tacctttaag accaatgact      240
200 tacaaggcag ctgtagatct tagccacttt ttaaaagaaa aggggggact ggaagggcta      300
201 attcactccc aacgaagaca agatatacct gatctgtgga tctaccacac acaaggctac      360
202 ttccttgatt ggcagaacta cacaccaggg ccagggggtca gatatacact gacctttgga      420
203 tgggtctaca agctagtacc agttgaagca gataaggtag aagaggccaa taaaggagag      480
204 aacaccagct ttttacaccc tgtgagcctg catggaatgg atgacctga gagagaagtg      540
205 tttagagtga ggtttgacag ccgcctagca ttcatcacg tggcccgaga gctgcatccg      600
206 gagtacttca agaactgcac tagtgagcca gtagatccta gactagagcc ctggaagcat      660
207 ccaggaagtc agcctaaaac tgcctgtacc aattgctatt gtaaaaagtg ttgctttcat      720
208 tgccaaagttt gtttcataac aaaagcctta gycatctcct atggcaggaa gaagcggaga      780
209 cagcgacgaa gacctcctca aggcagtcag actcatcaag tttctctatc aaagcaaccc      840
210 acctcccaat cccgagggga cccgacaggc ccgaaggaaa ctagtggcca ccatcaccat      900
211 caccattaa
213 <210> SEQ ID NO: 13
214 <211> LENGTH: 302
215 <212> TYPE: PRT
216 <213> ORGANISM: Pichia pastoris
217 <400> SEQUENCE: 13
219 Met Gly Gly Lys Trp Ser Lys Ser Ser Val Val Gly Trp Pro Thr Val
220 1          5          10          15
221 Arg Glu Arg Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly Ala
222                20                25                30
223 Ala Ser Arg Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn Thr
224                35                40                45
225 Ala Ala Thr Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu Glu
226                50                55                60
227 Glu Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr
228 65                70                75                80
229 Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly
230                85                90                95

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231 Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu
 232 100 105 110
 233 Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr
 234 115 120 125
 235 Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys
 236 130 135 140
 237 Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu
 238 145 150 155 160
 239 Asn Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp Asp Pro
 240 165 170 175
 241 Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His
 242 180 185 190
 243 His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser
 244 195 200 205
 245 Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser Gln
 246 210 215 220
 247 Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His
 248 225 230 235 240
 249 Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly Arg
 250 245 250 255
 251 Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr His
 252 260 265 270
 253 Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Arg Gly Asp Pro
 254 275 280 285
 255 Thr Gly Pro Lys Glu Thr Ser Gly His His His His His His
 256 290 295 300

258 <210> SEQ ID NO: 14

259 <211> LENGTH: 1029

260 <212> TYPE: DNA

261 <213> ORGANISM: Pichia pastoris

263 <400> SEQUENCE: 14

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265 agccattcat caaatatggc gaatacccaa atgaaatcag acaaaatcat tattgctcac	120
266 cgtggtgcta gcggttattt accagagcat acgttagaat ctaaagcact tgccttttgca	180
267 caacaggtcg attatttaga gcaagattta gcaatgacta aggatggtcg tttagtgggt	240
268 attcacgata acttttttaga tggcttgact gatgttgcca aaaaattccc acatcgatcat	300
269 cgtaaagatg gccgttacta tgtcatcgac ttacacctaa aagaaattca agttagtaga	360
270 atgacagaaa actttgaaac catgggtggc aagtgggtcaa aaagttagtg ggttggatgg	420
271 cctactgtaa gggaaagaat gagacgagct gagccagcag cagatggggt gggagcagca	480
272 tctcgagacc tggaaaaaca tggagcaatc acaagtagca atacagcagc taccaatgct	540
273 gcttgtgctt ggctagaagc acaagaggag gaggagggtg gttttccagt cacacctcag	600
274 gtacctttta gaccaatgac ttacaaggca gctgtagatc ttageccactt tttaaaagaa	660
275 aaggggggac tggaaaggct aattcaactc caacgaagac aagatatact tgatctgtgg	720
276 atctaccaca cacaaggcta ctccctgat tggcagaact acacaccagg gccaggggtc	780
277 agatatccac tgacctttgg atggtgttac aagctagtag cagtttagcc agataaggta	840
278 gaagaggcca ataaaggaga gaacaccagc ttgttacacc ctgtgagcct gcatggaatg	900
279 gatgacctg agagagaagt gtttagatgg aggtttgaca gccgcctagc atttcatcac	960
280 gtggcccgag agctgcatcc ggagtacttc aagaactgca ctagtggcca ccatcaccat	1020
281 caccattaa	1029

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VERIFICATION SUMMARY

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